SEQUENCE LISTING

<110> Umana, Pablo
Bruenker, Peter
Ferrara, Claudia
Suter, Tobias

<120> Fusion Constructs and Use of Same to Produce Antibodies with Increased Fc Receptor Binding Affinity and Effector Function

<130> 1975.0180003

<150> US 60/441,307
<151> 2003-01-22

<150> US 60/491,254
<151> 2003-07-31

<150> US 60/495,142
<151> 2003-08-15

<160> 20

<170> PatentIn version 3.2

<210> 1
<211> 11
<212> PRT
<213> Unknown

<220>
<223> c-myc epitope tag

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Pro Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
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ttcgg 65

<210> 8
<211> 66
<212> DNA
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tccgaaaagt tcacaaagca atttcagcca aggtgctggc tcacccctgc tccagccact 60

gtcccc 66

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<212> DNA
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<223> GAB-255 PCR primer

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<223> GAB-261 PCR primer

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<210> 11
<211> 48
<212> DNA
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<211> 1715
<212> DNA
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<223> Nucleotide sequence of GnTI-GnTIII

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ggctccttcc ctcagggcca gctctcaatg ttgcaagaaa aaatagacca tttggagcgt 180

ttgctagctg agaataatga gatcatctca aatattagag actcagtcat caatttgagt 240

gagtctgtgg aggatggtcc gaaaagttca caaagcaatt tcagccaagg tgctggctca 300

cccctgctcc agccactgtc ccctagcaag gccaccgaag aactgcaccg ggtggacttc 360

gtgttgccgg aggacaccac agagtatttt gtgcgcacca aagctggcgg tgtgtgcttc 420

aaaccaggta ccaggatgct ggagaaacct tctccagggc ggacagagga gaagaccaag 480

gtggctgagg ggtcctcggt ccggggtcct gctcggaggc ctatgcggca tgtgttgagt 540

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accagggctc agacggaagg tcatctgctg tcaggggcaa gttggataca acggagggcc 1680

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<212> PRT
<213> Artificial Sequence

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<223> Amino acid sequence of GnTI-GnTIII

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Val Val Ile Phe Ser Leu Tyr Leu Met Leu Asp Arg Gly His Leu Asp
20 25 30

Tyr Pro Arg Asn Pro Arg Arg Glu Gly Ser Phe Pro Gln Gly Gln Leu

35 40 45

Ser Met Leu Gln Glu Lys Ile Asp His Leu Glu Arg Leu Leu Ala Glu
50 55 60

Asn Asn Glu Ile Ile Ser Asn Ile Arg Asp Ser Val Ile Asn Leu Ser
65 70 75 80

Glu Ser Val Glu Asp Gly Pro Lys Ser Ser Gln Ser Asn Phe Ser Gln
85 90 95

Gly Ala Gly Ser Pro Leu Leu Gln Pro Leu Ser Pro Ser Lys Ala Thr
100 105 110

Glu Glu Leu His Arg Val Asp Phe Val Leu Pro Glu Asp Thr Thr Glu
115 120 125

Tyr Phe Val Arg Thr Lys Ala Gly Gly Val Cys Phe Lys Pro Gly Thr
130 135 140

Arg Met Leu Glu Lys Pro Ser Pro Gly Arg Thr Glu Glu Lys Thr Lys
145 150 155 160

Val Ala Glu Gly Ser Ser Val Arg Gly Pro Ala Arg Arg Pro Met Arg
165 170 175

His Val Leu Ser Ala Arg Glu Arg Leu Gly Gly Arg Gly Thr Arg Arg
180 185 190

Lys Trp Val Glu Cys Val Cys Leu Pro Gly Trp His Gly Pro Ser Cys
195 200 205

Gly Val Pro Thr Val Val Gln Tyr Ser Asn Leu Pro Thr Lys Glu Arg
210 215 220

Leu Val Pro Arg Glu Val Pro Arg Arg Val Ile Asn Ala Ile Asn Ile
225 230 235 240

Asn His Glu Phe Asp Leu Leu Asp Val Arg Phe His Glu Leu Gly Asp
245 250 255

Val Val Asp Ala Phe Val Val Cys Glu Ser Asn Phe Thr Ala Tyr Gly
260 265 270

Glu Pro Arg Pro Leu Lys Phe Arg Glu Met Leu Thr Asn Gly Thr Phe
275 280 285

Glu Tyr Ile Arg His Lys Val Leu Tyr Val Phe Leu Asp His Phe Pro
290 295 300

Pro Gly Gly Arg Gln Asp Gly Trp Ile Ala Asp Asp Tyr Leu Arg Thr
305 310 315 320

Phe Leu Thr Gln Asp Gly Val Ser Arg Leu Arg Asn Leu Arg Pro Asp
325 330 335

Asp Val Phe Ile Ile Asp Asp Ala Asp Glu Ile Pro Ala Arg Asp Gly
340 345 350

Val Leu Phe Leu Lys Leu Tyr Asp Gly Trp Thr Glu Pro Phe Ala Phe
355 360 365

His Met Arg Lys Ser Leu Tyr Gly Phe Phe Trp Lys Gln Pro Gly Thr
370 375 380

Leu Glu Val Val Ser Gly Cys Thr Ile Asp Met Leu Gln Ala Val Tyr
385 390 395 400

Gly Leu Asp Gly Ile Arg Leu Arg Arg Arg Gln Tyr Tyr Thr Met Pro
405 410 415

Asn Phe Arg Gln Tyr Glu Asn Arg Thr Gly His Ile Leu Val Gln Trp
420 425 430

Ser Leu Gly Ser Pro Leu His Phe Ala Gly Trp His Cys Ser Trp Cys
435 440 445

Phe Thr Pro Glu Gly Ile Tyr Phe Lys Leu Val Ser Ala Gln Asn Gly
450 455 460

Asp Phe Pro Arg Trp Gly Asp Tyr Glu Asp Lys Arg Asp Leu Asn Tyr
465 470 475 480

Ile Arg Ser Leu Ile Arg Thr Gly Gly Trp Phe Asp Gly Thr Gln Gln
485 490 495

Glu Tyr Pro Pro Ala Asp Pro Ser Glu His Met Tyr Ala Pro Lys Tyr
500 505 510

Leu Leu Lys Asn Tyr Asp Gln Phe Arg Tyr Leu Leu Glu Asn Pro Tyr
515 520 525

Arg Glu Pro Lys Ser Thr Val Glu Gly Gly Arg Arg Asn Gln Gly Ser
530 535 540

Asp Gly Arg Ser Ser Ala Val Arg Gly Lys Leu Asp Thr Thr Glu Gly
545 550 555 560

Pro Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
565 570

<210> 14
<211> 1722
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of ManII-GnTIII

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agcgctctcg atggcgaccc cgccagcctc acccgggaag tgattcgcct ggcccaagac 180

gccgaggtgg agctggagcg gcagcgtggg ctgctgcagc agatcgggga tgccctgtcg 240

agccagcggg ggagggtgcc caccgcggcc cctcccgccc agccgcgtgt gcctgtgacc 300

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tgcttcaaac caggtaccag gatgctggag aaaccttctc cagggcggac agaggagaag 480

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cgccggaacc agggctcaga cggaaggtca tctgctgtca ggggcaagtt ggatacaacg 1680

gagggcccgg aacagaaact gatctctgaa gaggacctgt ag 1722

<210> 15
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of ManII-GnTIII fusion

<400> 15

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20 25 30

Ala Pro Gly Arg Pro Pro Ser Val Ser Ala Leu Asp Gly Asp Pro Ala
35 40 45

Ser Leu Thr Arg Glu Val Ile Arg Leu Ala Gln Asp Ala Glu Val Glu
50 55 60

Leu Glu Arg Gln Arg Gly Leu Leu Gln Gln Ile Gly Asp Ala Leu Ser
65 70 75 80

Ser Gln Arg Gly Arg Val Pro Thr Ala Ala Pro Pro Ala Gln Pro Arg
85 90 95

Val Pro Val Thr Pro Ala Pro Leu Leu Gln Pro Leu Ser Pro Ser Lys
100 105 110

Ala Thr Glu Glu Leu His Arg Val Asp Phe Val Leu Pro Glu Asp Thr
115 120 125

Thr Glu Tyr Phe Val Arg Thr Lys Ala Gly Gly Val Cys Phe Lys Pro
130 135 140

Gly Thr Arg Met Leu Glu Lys Pro Ser Pro Gly Arg Thr Glu Glu Lys

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145                 150                 155                 160

Thr Lys Val Ala Glu Gly Ser Ser Val Arg Gly Pro Ala Arg Arg Pro
                165                 170                 175

Met Arg His Val Leu Ser Ala Arg Glu Arg Leu Gly Gly Arg Gly Thr
            180                 185                 190

Arg Arg Lys Trp Val Glu Cys Val Cys Leu Pro Gly Trp His Gly Pro
        195                 200                 205

Ser Cys Gly Val Pro Thr Val Val Gln Tyr Ser Asn Leu Pro Thr Lys
    210                 215                 220

Glu Arg Leu Val Pro Arg Glu Val Pro Arg Arg Val Ile Asn Ala Ile
225                 230                 235                 240

Asn Ile Asn His Glu Phe Asp Leu Leu Asp Val Arg Phe His Glu Leu
                245                 250                 255

Gly Asp Val Val Asp Ala Phe Val Val Cys Glu Ser Asn Phe Thr Ala
            260                 265                 270

Tyr Gly Glu Pro Arg Pro Leu Lys Phe Arg Glu Met Leu Thr Asn Gly
        275                 280                 285

Thr Phe Glu Tyr Ile Arg His Lys Val Leu Tyr Val Phe Leu Asp His
    290                 295                 300

Phe Pro Pro Gly Gly Arg Gln Asp Gly Trp Ile Ala Asp Asp Tyr Leu
305                 310                 315                 320

Arg Thr Phe Leu Thr Gln Asp Gly Val Ser Arg Leu Arg Asn Leu Arg
                325                 330                 335

Pro Asp Asp Val Phe Ile Ile Asp Asp Ala Asp Glu Ile Pro Ala Arg
            340                 345                 350

Asp Gly Val Leu Phe Leu Lys Leu Tyr Asp Gly Trp Thr Glu Pro Phe
        355                 360                 365

Ala Phe His Met Arg Lys Ser Leu Tyr Gly Phe Phe Trp Lys Gln Pro
    370                 375                 380

Gly Thr Leu Glu Val Val Ser Gly Cys Thr Ile Asp Met Leu Gln Ala
385                 390                 395                 400
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Val Tyr Gly Leu Asp Gly Ile Arg Leu Arg Arg Arg Gln Tyr Tyr Thr
                405                 410                 415

Met Pro Asn Phe Arg Gln Tyr Glu Asn Arg Thr Gly His Ile Leu Val
            420                 425                 430

Gln Trp Ser Leu Gly Ser Pro Leu His Phe Ala Gly Trp His Cys Ser
        435                 440                 445

Trp Cys Phe Thr Pro Glu Gly Ile Tyr Phe Lys Leu Val Ser Ala Gln
    450                 455                 460

Asn Gly Asp Phe Pro Arg Trp Gly Asp Tyr Glu Asp Lys Arg Asp Leu
465                 470                 475                 480

Asn Tyr Ile Arg Ser Leu Ile Arg Thr Gly Gly Trp Phe Asp Gly Thr
                485                 490                 495

Gln Gln Glu Tyr Pro Pro Ala Asp Pro Ser Glu His Met Tyr Ala Pro
            500                 505                 510

Lys Tyr Leu Leu Lys Asn Tyr Asp Gln Phe Arg Tyr Leu Leu Glu Asn
        515                 520                 525

Pro Tyr Arg Glu Pro Lys Ser Thr Val Glu Gly Gly Arg Arg Asn Gln
    530                 535                 540

Gly Ser Asp Gly Arg Ser Ser Ala Val Arg Gly Lys Leu Asp Thr Thr
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Glu Gly Pro Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
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<223> GalT amino acid sequence from pBlueGalT

<400> 16

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Ala Ser Leu Gln Arg Ala Cys Arg Leu Leu Val Ala Val Cys Ala Leu
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His Leu Gly Val Thr Leu Val Tyr Tyr Leu Ala Gly Arg Asp Leu Ser
        35                  40                  45

Arg Leu Pro Gln Leu Val Gly Val Ser Thr Pro Leu Gln Gly Gly Ser
    50                  55                  60

Asn Ser Ala Ala Ala Ile Gly Gln Ser Ser Gly Glu Leu Arg Thr Gly
65                  70                  75                  80

Gly Ala Arg Pro Pro Pro Pro Leu Gly Ala Ser Ser Gln Pro Arg Pro
                85                  90                  95

Gly Gly Asp Ser Ser Pro Val Val Asp Ser Gly Pro Gly Pro Ala Ser
            100                 105                 110

Asn Leu Thr Ser Val Pro Val Pro His Thr Thr Ala Leu Ser Leu Pro
        115                 120                 125

Ala Cys Pro Glu Glu Ser Pro Leu Leu Val Gly Pro Met Leu Ile Glu
    130                 135                 140

Phe Asn Met Pro Val Asp Leu Glu Leu Val Ala Lys Gln Asn Pro Asn
145                 150                 155                 160

Val Lys Met Gly Gly Arg Tyr Ala Pro Arg Asp Cys Val Ser Pro His
                165                 170                 175

Lys Val Ala Ile Ile Ile Pro Phe Arg Asn Arg Gln Glu His Leu Lys
            180                 185                 190

Tyr Trp Leu Tyr Tyr Leu His Pro Val Leu Gln Arg Gln Gln Leu Asp
        195                 200                 205

Tyr Gly Ile Tyr Val Ile Asn Gln Ala Gly Asp Thr Ile Phe Asn Arg
    210                 215                 220

Ala Lys Leu Leu Asn Val Gly Phe Gln Glu Ala Leu Lys Asp Tyr Asp
225                 230                 235                 240

Tyr Thr Cys Phe Val Phe Ser Asp Val Asp Leu Ile Pro Met Asn Asp
                245                 250                 255

His Asn Ala Tyr Arg Cys Phe Ser Gln Pro Arg His Ile Ser Val Ala
            260                 265                 270

Met Asp Lys Phe Gly Phe Ser Leu Pro Tyr Val Gln Tyr Phe Gly Gly
        275                 280                 285
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Val Ser Ala Leu Ser Lys Gln Gln Phe Leu Thr Ile Asn Gly Phe Pro
290 295 300

Asn Asn Tyr Trp Gly Trp Gly Gly Glu Asp Asp Asp Ile Phe Asn Arg
305 310 315 320

Leu Val Phe Arg Gly Met Ser Ile Ser Arg Pro Asn Ala Val Val Gly
325 330 335

Arg Cys Arg Met Ile Arg His Ser Arg Asp Lys Lys Asn Glu Pro Asn
340 345 350

Pro Gln Arg Phe Asp Arg Ile Ala His Thr Lys Glu Thr Met Leu Ser
355 360 365

Asp Gly Leu Asn Ser Leu Thr Tyr Gln Val Leu Asp Val Gln Arg Tyr
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Pro Leu Tyr Thr Gln Ile Thr Val Asp Ile Gly Thr Pro Ser
385 390 395

<210> 17
<211> 3435
<212> DNA
<213> Homo sapiens

<400> 17
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ggctccttcc ctcagggcca gctctcaatg ttgcaagaaa aaatagacca tttggagcgt 180

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gacaatccag atggtggagt ttggaagcaa ggatttgaca ttacttatga atctaatgaa 480

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ttaaacaagt ttattgtcga aagtctcaca ccttcatcac tatccttgat gcattcacct 3360

cccggcactc agaatataag tgagatcaac ttgagtccaa tggaaatcag cacattccga 3420

atccagttga ggtga 3435

<210> 18
<211> 1144
<212> PRT
<213> Homo sapiens

<400> 18

Met Lys Leu Ser Arg Gln Phe Thr Val Phe Gly Ser Ala Ile Phe Cys
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Val Val Ile Phe Ser Leu Tyr Leu Met Leu Asp Arg Gly His Leu Asp
20 25 30

Tyr Pro Arg Asn Pro Arg Arg Glu Gly Ser Phe Pro Gln Gly Gln Leu
35 40 45

Ser Met Leu Gln Glu Lys Ile Asp His Leu Glu Arg Leu Leu Ala Glu
50 55 60

Asn Asn Glu Ile Ile Ser Asn Ile Arg Asp Ser Val Ile Asn Leu Ser
65 70 75 80

Glu Ser Val Glu Asp Gly Pro Lys Ser Ser Gln Ser Asn Phe Ser Gln
85 90 95

Gly Ala Gly Ser His Leu Leu Pro Ser Gln Leu Ser Leu Ser Val Asp
100 105 110

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Thr Ala Asp Cys Leu Phe Ala Ser Gln Ser Gly Ser His Asn Ser Asp
        115                 120                 125

Val Gln Met Leu Asp Val Tyr Ser Leu Ile Ser Phe Asp Asn Pro Asp
    130                 135                 140

Gly Gly Val Trp Lys Gln Gly Phe Asp Ile Thr Tyr Glu Ser Asn Glu
145                 150                 155                 160

Trp Asp Thr Glu Pro Leu Gln Val Phe Val Val Pro His Ser His Asn
                165                 170                 175

Asp Pro Gly Trp Leu Lys Thr Phe Asn Asp Tyr Phe Arg Asp Lys Thr
            180                 185                 190

Gln Tyr Ile Phe Asn Asn Met Val Leu Lys Leu Lys Glu Asp Ser Arg
        195                 200                 205

Arg Lys Phe Ile Trp Ser Glu Ile Ser Tyr Leu Ser Lys Trp Trp Asp
    210                 215                 220

Ile Ile Asp Ile Gln Lys Lys Asp Ala Val Lys Ser Leu Ile Glu Asn
225                 230                 235                 240

Gly Gln Leu Glu Ile Val Thr Gly Gly Trp Val Met Pro Asp Glu Ala
                245                 250                 255

Thr Pro His Tyr Phe Ala Leu Ile Asp Gln Leu Ile Glu Gly His Gln
            260                 265                 270

Trp Leu Glu Asn Asn Ile Gly Val Lys Pro Arg Ser Gly Trp Ala Ile
        275                 280                 285

Asp Pro Phe Gly His Ser Pro Thr Met Ala Tyr Leu Leu Asn Arg Ala
    290                 295                 300

Gly Leu Ser His Met Leu Ile Gln Arg Val His Tyr Ala Val Lys Lys
305                 310                 315                 320

His Phe Ala Leu His Lys Thr Leu Glu Phe Phe Trp Arg Gln Asn Trp
                325                 330                 335

Asp Leu Gly Ser Val Thr Asp Ile Leu Cys His Met Met Pro Phe Tyr
            340                 345                 350

Ser Tyr Asp Ile Pro His Thr Cys Gly Pro Asp Pro Lys Ile Cys Cys
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        355                 360                 365

Gln Phe Asp Phe Lys Arg Leu Pro Gly Gly Arg Phe Gly Cys Pro Trp
    370                 375                 380

Gly Val Pro Pro Glu Thr Ile His Pro Gly Asn Val Gln Ser Arg Ala
385                 390                 395                 400

Arg Met Leu Leu Asp Gln Tyr Arg Lys Lys Ser Lys Leu Phe Arg Thr
                405                 410                 415

Lys Val Leu Leu Ala Pro Leu Gly Asp Asp Phe Arg Tyr Cys Glu Tyr
            420                 425                 430

Thr Glu Trp Asp Leu Gln Phe Lys Asn Tyr Gln Gln Leu Phe Asp Tyr
        435                 440                 445

Met Asn Ser Gln Ser Lys Phe Lys Val Lys Ile Gln Phe Gly Thr Leu
    450                 455                 460

Ser Asp Phe Phe Asp Ala Leu Asp Lys Ala Asp Glu Thr Gln Arg Asp
465                 470                 475                 480

Lys Gly Gln Ser Met Phe Pro Val Leu Ser Gly Asp Phe Phe Thr Tyr
                485                 490                 495

Ala Asp Arg Asp Asp His Tyr Trp Ser Gly Tyr Phe Thr Ser Arg Pro
            500                 505                 510

Phe Tyr Lys Arg Met Asp Arg Ile Met Glu Ser His Leu Arg Ala Ala
        515                 520                 525

Glu Ile Leu Tyr Tyr Phe Ala Leu Arg Gln Ala His Lys Tyr Lys Ile
    530                 535                 540

Asn Lys Phe Leu Ser Ser Ser Leu Tyr Thr Ala Leu Thr Glu Ala Arg
545                 550                 555                 560

Arg Asn Leu Gly Leu Phe Gln His His Asp Ala Ile Thr Gly Thr Ala
                565                 570                 575

Lys Asp Trp Val Val Val Asp Tyr Gly Thr Arg Leu Phe His Ser Leu
            580                 585                 590

Met Val Leu Glu Lys Ile Ile Gly Asn Ser Ala Phe Leu Leu Ile Leu
        595                 600                 605
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Lys Asp Lys Leu Thr Tyr Asp Ser Tyr Ser Pro Asp Thr Phe Leu Glu
610 615 620

Met Asp Leu Lys Gln Lys Ser Gln Asp Ser Leu Pro Gln Lys Asn Ile
625 630 635 640

Ile Arg Leu Ser Ala Glu Pro Arg Tyr Leu Val Val Tyr Asn Pro Leu
645 650 655

Glu Gln Asp Arg Ile Ser Leu Val Ser Val Tyr Val Ser Ser Pro Thr
660 665 670

Val Gln Val Phe Ser Ala Ser Gly Lys Pro Val Glu Val Gln Val Ser
675 680 685

Ala Val Trp Asp Thr Ala Asn Thr Ile Ser Glu Thr Ala Tyr Glu Ile
690 695 700

Ser Phe Arg Ala His Ile Pro Pro Leu Gly Leu Lys Val Tyr Lys Ile
705 710 715 720

Leu Glu Ser Ala Ser Ser Asn Ser His Leu Ala Asp Tyr Val Leu Tyr
725 730 735

Lys Asn Lys Val Glu Asp Ser Gly Ile Phe Thr Ile Lys Asn Met Ile
740 745 750

Asn Thr Glu Glu Gly Ile Thr Leu Glu Asn Ser Phe Val Leu Leu Arg
755 760 765

Phe Asp Gln Thr Gly Leu Met Lys Gln Met Met Thr Lys Glu Asp Gly
770 775 780

Lys His His Glu Val Asn Val Gln Phe Ser Trp Tyr Gly Thr Thr Ile
785 790 795 800

Lys Arg Asp Lys Ser Gly Ala Tyr Leu Phe Leu Pro Asp Gly Asn Ala
805 810 815

Lys Pro Tyr Val Tyr Thr Thr Pro Pro Phe Val Arg Val Thr His Gly
820 825 830

Arg Ile Tyr Ser Glu Val Thr Cys Phe Phe Asp His Val Thr His Arg
835 840 845

Val Arg Leu Tyr His Ile Gln Gly Ile Glu Gly Gln Ser Val Glu Val

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     850                 855                 860

Ser Asn Ile Val Asp Ile Arg Lys Val Tyr Asn Arg Glu Ile Ala Met
865                 870                 875                 880

Lys Ile Ser Ser Asp Ile Lys Ser Gln Asn Arg Phe Tyr Thr Asp Leu
                885                 890                 895

Asn Gly Tyr Gln Ile Gln Pro Arg Met Thr Leu Ser Lys Leu Pro Leu
            900                 905                 910

Gln Ala Asn Val Tyr Pro Met Thr Thr Met Ala Tyr Ile Gln Asp Ala
        915                 920                 925

Lys His Arg Leu Thr Leu Leu Ser Ala Gln Ser Leu Gly Val Ser Ser
    930                 935                 940

Leu Asn Ser Gly Gln Ile Glu Val Ile Met Asp Arg Arg Leu Met Gln
945                 950                 955                 960

Asp Asp Asn Arg Gly Leu Glu Gln Gly Ile Gln Asp Asn Lys Ile Thr
                965                 970                 975

Ala Asn Leu Phe Arg Ile Leu Leu Glu Lys Arg Ser Ala Val Asn Thr
            980                 985                 990

Glu Glu Glu Lys Lys Ser Val Ser  Tyr Pro Ser Leu Leu  Ser His Ile
        995                 1000                1005

Thr Ser  Ser Leu Met Asn His  Pro Val Ile Pro Met  Ala Asn Lys
    1010                1015                1020

Phe Phe  Ser Pro Thr Leu Glu  Leu Gln Gly Glu Phe  Ser Pro Leu
    1025                1030                1035

Gln Ser  Ser Leu Pro Cys Asp  Ile His Leu Val Asn  Leu Arg Thr
    1040                1045                1050

Ile Gln  Ser Lys Val Gly Asn  Gly His Ser Asn Glu  Ala Ala Leu
    1055                1060                1065

Ile Leu  His Arg Lys Gly Phe  Asp Cys Arg Phe Ser  Ser Lys Gly
    1070                1075                1080

Thr Gly  Leu Phe Cys Ser Thr  Thr Gln Gly Lys Ile  Leu Val Gln
    1085                1090                1095
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Lys Leu Leu Asn Lys Phe Ile Val Glu Ser Leu Thr Pro Ser Ser
1100 1105 1110

Leu Ser Leu Met His Ser Pro Pro Gly Thr Gln Asn Ile Ser Glu
1115 1120 1125

Ile Asn Leu Ser Pro Met Glu Ile Ser Thr Phe Arg Ile Gln Leu
1130 1135 1140

Arg

<210> 19
<211> 1116
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of ManII-GalT

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tcgctctacc tgatgctgga ccggggtcac ttagactacc ccaggaaccc gcgccgcgag 120

ggctccttcc ctcagggcca gctctcaatg ttgcaagaaa aaatagacca tttggagcgt 180

ttgctagctg agaataatga gatcatctca aatattagag actcagtcat caatttgagt 240

gagtctgtgg aggatggtcc gaaaagttca caaagcaatt tcagccaagg tgctggctca 300

cccgcctgcc ctgaggagtc cccgctgctt gtgggcccca tgctgattga gtttaacatg 360

cctgtggacc tggagctcgt ggcaaagcag aacccaaatg tgaagatggg cggccgctat 420

gcccccaggg actgcgtctc tcctcacaag gtggccatca tcattccatt ccgcaaccgg 480

caggagcacc tcaagtactg gctatattat ttgcacccag tcctgcagcg ccagcagctg 540

gactatggca tctatgttat caaccaggcg ggagacacta tattcaatcg tgctaagctc 600

ctcaatgttg gctttcaaga agccttgaag gactatgact acacctgctt tgtgtttagt 660

gacgtggacc tcattccaat gaatgaccat aatgcgtaca ggtgtttttc acagccacgg 720

cacatttccg ttgcaatgga taagtttgga ttcagcctac cttatgttca gtattttgga 780

ggtgtctctg ctctaagtaa acaacagttt ctaaccatca atggatttcc taataattat 840

tggggctggg gaggagaaga tgatgacatt tttaacagat tagtttttag aggcatgtct 900

atatctcgcc caaatgctgt ggtcgggagg tgtcgcatga tccgccactc aagagacaaa 960

aaaaatgaac ccaatcctca gaggtttgac cgaattgcac acacaaagga gacaatgctc 1020

tctgatggtt tgaactcact cacctaccag gtgctggatg tacagagata cccattgtat 1080

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<211> 371
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of ManII-GalT

<400> 20

Met Lys Leu Ser Arg Gln Phe Thr Val Phe Gly Ser Ala Ile Phe Cys
1 5 10 15

Val Val Ile Phe Ser Leu Tyr Leu Met Leu Asp Arg Gly His Leu Asp
20 25 30

Tyr Pro Arg Asn Pro Arg Arg Glu Gly Ser Phe Pro Gln Gly Gln Leu
35 40 45

Ser Met Leu Gln Glu Lys Ile Asp His Leu Glu Arg Leu Leu Ala Glu
50 55 60

Asn Asn Glu Ile Ile Ser Asn Ile Arg Asp Ser Val Ile Asn Leu Ser
65 70 75 80

Glu Ser Val Glu Asp Gly Pro Lys Ser Ser Gln Ser Asn Phe Ser Gln
85 90 95

Gly Ala Gly Ser Pro Ala Cys Pro Glu Glu Ser Pro Leu Leu Val Gly
100 105 110

Pro Met Leu Ile Glu Phe Asn Met Pro Val Asp Leu Glu Leu Val Ala
115 120 125

Lys Gln Asn Pro Asn Val Lys Met Gly Gly Arg Tyr Ala Pro Arg Asp
130 135 140

Cys Val Ser Pro His Lys Val Ala Ile Ile Ile Pro Phe Arg Asn Arg
145 150 155 160

Gln Glu His Leu Lys Tyr Trp Leu Tyr Tyr Leu His Pro Val Leu Gln
165 170 175

Arg Gln Gln Leu Asp Tyr Gly Ile Tyr Val Ile Asn Gln Ala Gly Asp
180 185 190

Thr Ile Phe Asn Arg Ala Lys Leu Leu Asn Val Gly Phe Gln Glu Ala
195 200 205

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Leu Lys Asp Tyr Asp Tyr Thr Cys Phe Val Phe Ser Asp Val Asp Leu
    210                 215                 220

Ile Pro Met Asn Asp His Asn Ala Tyr Arg Cys Phe Ser Gln Pro Arg
225                 230                 235                 240

His Ile Ser Val Ala Met Asp Lys Phe Gly Phe Ser Leu Pro Tyr Val
                245                 250                 255

Gln Tyr Phe Gly Gly Val Ser Ala Leu Ser Lys Gln Gln Phe Leu Thr
            260                 265                 270

Ile Asn Gly Phe Pro Asn Asn Tyr Trp Gly Trp Gly Gly Glu Asp Asp
        275                 280                 285

Asp Ile Phe Asn Arg Leu Val Phe Arg Gly Met Ser Ile Ser Arg Pro
    290                 295                 300

Asn Ala Val Val Gly Arg Cys Arg Met Ile Arg His Ser Arg Asp Lys
305                 310                 315                 320

Lys Asn Glu Pro Asn Pro Gln Arg Phe Asp Arg Ile Ala His Thr Lys
                325                 330                 335

Glu Thr Met Leu Ser Asp Gly Leu Asn Ser Leu Thr Tyr Gln Val Leu
            340                 345                 350

Asp Val Gln Arg Tyr Pro Leu Tyr Thr Gln Ile Thr Val Asp Ile Gly
        355                 360                 365

Thr Pro Ser
    370
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